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What is claimed is:

1. An array comprising of any 10 or more nucleic acid probes containing 9 or more consecutive nucleotides from the sequences listed in SEQ ID NOS: 1-127811, or the perfect match, perfect mismatch, antisense match or antisense mismatch thereof.

2. The array of claim 1 comprising any 100 or more nucleic acid probes containing 9 or more consecutive nucleotides from the sequences listed in SEQ ID NOS: 1-127811, or the perfect match, perfect mismatch, antisense match or antisense mismatch thereof.

3. The array of claim 1 comprising any 1000 or more nucleic acid probes containing 9 or more consecutive nucleotides from the sequences listed in SEQ ID NOS: 1-127811, or the perfect match, perfect mismatch, antisense match or antisense mismatch thereof.

4. The array of claim 1 comprising any 10,000 or more nucleic acid probes containing 9 or more consecutive nucleotides from the sequences listed in SEQ ID NOS: 1-127811, or the perfect match, perfect mismatch, antisense match or antisense mismatch thereof.

5. The array of claim 1 comprising any 100,000 or more nucleic acid probes containing 9 or more consecutive nucleotides from the sequences listed in SEQ ID NOS: 1-127811, or the perfect match, perfect mismatch, antisense match or antisense mismatch thereof.

6. The array of claim 1 wherein said array is used to monitor gene expression levels.

7. The array of claim 1 wherein said array is used to monitor gene expression levels by hybridization to a DNA library.

8. The array of claim 1 wherein said array is used to monitor gene expression levels by hybridization to an mRNA-protein fusion compound.

9. The array of claim 1 wherein said array is used for analysis of genetic selections.

10. The array of claim 1 wherein said array is used for identification of polymorphisms.

11. The array of claim 1 wherein said array is used for identification of biallelic markers.

12. The array of claim 1 wherein said array is used for the production of genetic maps.

13. The array of claim 1 wherein said array is used for analysis of genetic variation.

14. The array of claim 1 wherein said array is used for comparative analysis of gene

expression in mouse and another species.

15. The array of claim 1 wherein said array is used to analyze a gene knockout.

16. The array of claim 1 wherein said array is used for hybridization of tag-labeled compounds.

17. A method of analysis comprising:

hybridizing one or more nucleic acids to 2 or more nucleic acid probes containing 9 or more consecutive nucleotides from the sequences listed in SEQ ID NOS: 1-127811, or the perfect match, perfect mismatch, antisense match or antisense mismatch thereof; and

detecting said hybridization.

18. The method of claim 17 wherein said hybridization is to 10 or more nucleic acid probes containing 9 or more consecutive nucleotides from the sequences listed in SEQ ID NOS: 1-127811, or the perfect match, perfect mismatch, antisense match or antisense mismatch thereof

19. The method of claim 17 wherein said hybridization is to 100 or more nucleic acid probes containing 9 or more consecutive nucleotides from the sequences listed in SEQ ID NOS: 1-127811, or the perfect match, perfect mismatch, antisense match or antisense mismatch thereof

20. The method of claim 17 wherein said hybridization is to 1000 or more nucleic acid probes containing 9 or more consecutive nucleotides from the sequences listed in SEQ ID NOS: 1-127811, or the perfect match, perfect mismatch, antisense match or antisense mismatch thereof

21. The method of claim 17 wherein said hybridization is to 10,000 or more nucleic acid probes containing 9 or more consecutive nucleotides from the sequences listed in SEQ ID NOS: 1-127811, or the perfect match, perfect mismatch, antisense match or antisense mismatch thereof

22. The method of claim 17 wherein said hybridization is to 100,000 or more nucleic acid probes containing 9 or more consecutive nucleotides from the sequences listed in SEQ ID NOS: 1-127811, or the perfect match, perfect mismatch, antisense match or antisense mismatch thereof

23. The method of claim 17 wherein said analysis comprises monitoring gene

expression levels.

24. The method of claim 18 wherein said nucleic acid probes containing 9 or more consecutive nucleotides from the sequences listed in SEQ ID NOS: 1-127811, or the perfect match, perfect mismatch, antisense match or antisense mismatch thereof are attached to an array.

25. The method of claim 23 wherein said monitoring gene expression levels comprises comparing gene expression levels of nucleic acids derived from two or more different samples and further comprises the step of:

comparing said hybridization patterns between said nucleic acids derived from said two or more different samples.

26. The method of claim 25 wherein said nucleic acid probes containing 9 or more consecutive nucleotides from the sequences listed in SEQ ID NOS: 1-127811, or the perfect match, perfect mismatch, antisense match or antisense mismatch thereof are attached to an array.

27. The method of claim 25 wherein at least one of said samples has been contacted with a drug.

28. The method of claim 27 wherein at least one of said samples is a control sample.

29. The method of claim 25 wherein at least one of said samples has been infected with a virus.

30. The method of claim 29 wherein at least one of said samples is an uninfected control sample.

31. The method of claim 25 wherein at least one of said samples is cancerous.

32. The method of claim 31 wherein one of said samples has been treated with a tumor suppressing drug.

33. The method of claim 17 wherein said analysis comprises analyzing the gene expression of samples exposed to selective conditions.

34. The method of claim 33 wherein said nucleic acid probes containing 9 or more consecutive nucleotides from the sequences listed in SEQ ID NOS: 1-127811, or the perfect match, perfect mismatch, antisense match or antisense mismatch thereof are attached to an array.

35. The method of claim 33 wherein at least one of said samples is derived from clones.

36. The method of claim 35 wherein said clones were derived from a two-hybrid analysis.

37. The method of claim 17 wherein at least one of said nucleic acids is part of a protein-mRNA fusion compound.

38. The method of claim 37 wherein said nucleic acid probes containing 9 or more consecutive nucleotides from the sequences listed in SEQ ID NOS: 1-127811, or the perfect match, perfect mismatch, antisense match or antisense mismatch thereof are attached to an array.

39. The method of claim 17 wherein said method of analysis comprises identifying biallelic markers.

40. The method of claim 39 wherein said nucleic acid probes containing 9 or more consecutive nucleotides from the sequences listed in SEQ ID NOS: 1-127811, or the perfect match, perfect mismatch, antisense match or antisense mismatch thereof are attached to an array.

41. The method of claim 40 wherein at least one of said nucleic acids is genomic nucleic acids.

42. The method of claim 17 wherein said method of analysis comprises identifying polymorphisms.

43. The method of claim 42 wherein said nucleic acid probes containing 9 or more consecutive nucleotides from the sequences listed in SEQ ID NOS: 1-127811, or the perfect match, perfect mismatch, antisense match or antisense mismatch thereof are attached to an array.

44. The method of claim 43 wherein at least one of said nucleic acids is genomic nucleic acids.

45. The method of claim 17 wherein said method of analysis comprises studying genetic variation.

46. The method of claim 45 wherein said nucleic acid probes containing 9 or more consecutive nucleotides from the sequences listed in SEQ ID NOS: 1-127811, or the perfect match, perfect mismatch, antisense match or antisense mismatch thereof are attached to an array.

47. The method of claim 45 wherein at least one of said nucleic acids is derived from phenotypically different strains of a species.

48. The method of claim 45 wherein at least one of said nucleic acids comprises genomic nucleic acids.

49. The method of claim 45 further comprising the step of developing markers from said hybridization pattern.

50. The method of claim 17 wherein said analysis comprises a cross-species comparison wherein the hybridization patterns of a pool of nucleic acids derived from one species are compared with the hybridization patterns of a pool of nucleic acids derived from another species.

51. The method of claim 50 wherein said nucleic acid probes containing 9 or more consecutive nucleotides from the sequences listed in SEQ ID NOS: 1-127811, or the perfect match, perfect mismatch, antisense match or antisense mismatch thereof are attached to an array.

52. The method of claim 17 wherein each of said nucleic acids further comprise a tag sequence.

53. The method of claim 52 wherein said tag sequences are derived from the nucleic acid probes containing 9 or more consecutive nucleotides from the sequences listed in SEQ ID NOS: 1-127811, or the perfect match, perfect mismatch, antisense match or antisense mismatch thereof.

54. The method of claim 52 wherein said nucleic acid probes containing 9 or more consecutive nucleotides from the sequences listed in SEQ ID NOS: 1-127811, or the perfect match, perfect mismatch, antisense match or antisense mismatch thereof are attached to an array.

55. The method of claim 52 wherein at least one of said nucleic acid sequences is derived from a deletion mutant.

56. The method of claim 17 wherein said analysis is a method of identifying family members of a gene.

57. The method of claim 56 wherein said nucleic acid probes containing 9 or more consecutive nucleotides from the sequences listed in SEQ ID NOS: 1-127811, or the perfect match, perfect mismatch, antisense match or antisense mismatch thereof are attached at an array.

58. The method of claim 56 wherein at least one of said nucleic acids is genomic nucleic acids.

59. A method comprising using any one or more of the nucleic acid probes containing 9 or more consecutive nucleotides from the sequences listed in SEQ ID NOS: 1-127811, or the perfect match, perfect mismatch, antisense match or antisense mismatch thereof as a primer for PCR to amplify a length of sequence from any one or more genes.

60. A method comprising using any one or more of the Table 1 sequences as a ligand to

any one or more genes

61. The method of claim 60 wherein said ligand is an antisense compound.

62. The method of claim 60 wherein said ligand prevents further binding to said gene.

63. The method of claim 60 wherein the purpose of said ligand is to inactivate said gene.

64. A method comprising using any one or more of the nucleic acid probes containing 9 or more consecutive nucleotides from the sequences listed in SEQ ID NOS: 1-127811, or the perfect match, perfect mismatch, antisense match or antisense mismatch thereof as a tag.

65. A method comprising using any one or more of the nucleic acid probes containing 9 or more consecutive nucleotides from the sequences listed in SEQ ID NOS: 1-127811, or the perfect match, perfect mismatch, antisense match or antisense mismatch thereof as a probe.

66. The method of claim 65 wherein said probe is used in an *in situ hybridization.*

67. The method of claim 65 wherein said probe is used to screen cDNA or genomic libraries, or subclones derived from them, for additional clones containing segments of DNA that have been isolated and previously sequenced.

68. The method of claim 65 wherein said probe is used in Southern, northern, or dot-blot hybridization to identify or detect the sequence of any gene.

69. The method of claim 65 wherein said probe is used in Southern or dot-blot hybridization of genomic DNA to detect specific mutations in any gene.

70. The method of claim 65 wherein said probe is used to detect specific mutations generated by site-directed mutagenesis of cloned genes.

71. The method of claim 65 wherein said probe is used to map the 5' termini of mRNA molecules by primer extensions.

72. The method of claim 65 wherein said probe is labeled.

73. The method of claim 72 wherein said probe is labeled with a phosphorescent label.

74. The method of claim 72 wherein said probe is labeled with a radioactive label.

75. The method of claim 72 wherein said probe is labeled with a flourescent label.

76. The method of claim 72 wherein said probe is labeled with a tag sequence.